03CO   0280   0IPE

CRF Errors Corrected by the STIC Systems Branch

CRF Processing Date: 12/17/2001
Edited by: _____
Verified by: _____ (STIC staf

Serial Number: 10/002,854   ENTERED   # 4

- [ ] Changed a file from non-ASCII to ASCII

- [ ] Changed the margins in cases where the sequence text was wrapped down to the next line.

- [ ] Edited a format error in the Current Application Data section, specifically: _____

- [ ] Edited the Current Application Data section with the actual current number. The number inputted by the applicant was: [ ] the prior application data; or [ ] other _____

- [ ] Added the mandatory heading and subheadings for "Current Application Data".

- [ ] Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

- [ ] Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

- [ ] Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

- [ ] Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

- [ ] Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

- [ ] Inserted colons after headings/subheadings. Headings edited included: _____

- [ ] Deleted extra, invalid, headings used by an applicant, specifically: _____

- [ ] Deleted: [ ] non-ASCII "garbage" at the beginning/end of files; [ ] secretary initials/filename at end of file; [ ] page numbers throughout text; [ ] other invalid text, such as _____

- [ ] Inserted mandatory headings, specifically: _____

- [ ] Corrected an obvious error in the response, specifically: _____

- [ ] Edited identifiers where upper case is used but lower case is required, or vice versa.

- [ ] Corrected an error in the Number of Sequences field, specifically: _____

- [ ] A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

- [ ] Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a Patentin bug). Sequences corrected: _____

- [✓] Other: Seq 2 - corrected amino acid numbering _____
  _____
  _____

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

```
                    RAW SEQUENCE LISTING                    DATE: 12/17/2001
                    PATENT APPLICATION:  US/10/002,854      TIME: 20:19:56

                    Input Set : A:\Pto.amc
                    Output Set: N:\CRF3\12172001\J002854.raw
```

```
 4 <110> APPLICANT: Scadden, David T.
 5        Poznansky, Mark C.
 6        Olszak, Ivona T.
 7        Brown, Edward M.
 9 <120> TITLE OF INVENTION: THE CaR RECEPTOR AS A MEDIATOR OF
10        MIGRATORY CELL CHEMOTAXIS AND/OR CHEMOKINESIS
13 <130> FILE REFERENCE: M0765/7038/ERG/KA
15 <140> CURRENT APPLICATION NUMBER: US/10/002,854
15 <141> CURRENT FILING DATE: 2001-11-01
15 <150> PRIOR APPLICATION NUMBER: PCT/US00/15440
16 <151> PRIOR FILING DATE: 2000-06-02
18 <160> NUMBER OF SEQ ID NOS: 2
20 <170> SOFTWARE: FastSEQ for Windows Version 3.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 3361
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (29)...(3262)
30 <223> OTHER INFORMATION: Ca-sensing Receptor
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33  tcccttgccc tggagagacg gcagaacc atg gca ttt tat agc tgc tgc tgg      52
34                                Met Ala Phe Tyr Ser Cys Cys Trp
35                                 1               5
37  gtc ctc ttg gca ctc acc tgg cac acc tct gcc tac ggg cca gac cag     100
38  Val Leu Leu Ala Leu Thr Trp His Thr Ser Ala Tyr Gly Pro Asp Gln
39       10                  15                  20
41  cga gcc caa aag aag ggg gac att atc ctt ggg ggg ctc ttt cct att     148
42  Arg Ala Gln Lys Lys Gly Asp Ile Ile Leu Gly Gly Leu Phe Pro Ile
43   25                  30                  35                  40
45  cat ttt gga gta gca gct aaa gat caa gat ctc aaa tca agg ccg gag     196
46  His Phe Gly Val Ala Ala Lys Asp Gln Asp Leu Lys Ser Arg Pro Glu
47                   45                  50                  55
49  tct gtg gaa tgt atc agg tat aat ttc cgt ggg ttt cgc tgg tta cag     244
50  Ser Val Glu Cys Ile Arg Tyr Asn Phe Arg Gly Phe Arg Trp Leu Gln
51               60                  65                  70
53  gct atg ata ttt gcc ata gag gag ata aac agc agc cca gcc ctt ctt     292
54  Ala Met Ile Phe Ala Ile Glu Glu Ile Asn Ser Ser Pro Ala Leu Leu
55           75                  80                  85
57  ccc aac ttg acg ctg gga tac agg ata ttt gac act tgc aac acc gtt     340
58  Pro Asn Leu Thr Leu Gly Tyr Arg Ile Phe Asp Thr Cys Asn Thr Val
59           90                  95                  100
61  tct aag gcc ttg gaa gcc acc ctg agt ttt gtt gct caa aac aaa att     388
62  Ser Lys Ala Leu Glu Ala Thr Leu Ser Phe Val Ala Gln Asn Lys Ile
63  105                  110                  115                  120
65  gat tct ttg aac ctt gat gag ttc tgc aac tgc tca gag cac att ccc     436
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                  RAW SEQUENCE LISTING              DATE: 12/17/2001
                  PATENT APPLICATION:  US/10/002,854 TIME: 20:19:56

                  Input Set : A:\Pto.amc
                  Output Set: N:\CRF3\12172001\J002854.raw

66  Asp Ser Leu Asn Leu Asp Glu Phe Cys Asn Cys Ser Glu His Ile Pro
67                125                 130                 135
69  tct acg att gct gtg gtg gga gca act ggc tca ggc gtc tcc acg gca    484
70  Ser Thr Ile Ala Val Val Gly Ala Thr Gly Ser Gly Val Ser Thr Ala
71                140                 145                 150
73  gtg gca aat ctg ctg ggg ctc tac att ccc cag gtc agt tat gcc        532
74  Val Ala Asn Leu Leu Gly Leu Phe Tyr Ile Pro Gln Val Ser Tyr Ala
75                155                 160                 165
77  tcc tcc agc aga ctc ctc agc aac aag aat caa ttc aag tct ttc ctc    580
78  Ser Ser Ser Arg Leu Leu Ser Asn Lys Asn Gln Phe Lys Ser Phe Leu
79                170                 175                 180
81  cga acc atc ccc aat gat gag cac cag gcc act gcc atg gca gac atc    628
82  Arg Thr Ile Pro Asn Asp Glu His Gln Ala Thr Ala Met Ala Asp Ile
83  185                 190                 195                 200
85  atc gag tat ttc cgc tgg aac tgg gtg ggc aca att gca gct gat gac    676
86  Ile Glu Tyr Phe Arg Trp Asn Trp Val Gly Thr Ile Ala Ala Asp Asp
87                205                 210                 215
89  gac tat ggg cgg ccg ggg att gag aaa ttc cga gag gaa gct gag gaa    724
90  Asp Tyr Gly Arg Pro Gly Ile Glu Lys Phe Arg Glu Glu Ala Glu Glu
91                220                 225                 230
93  agg gat atc tgc atc gac ttc agt gaa ctc atc tcc cag tac tct gat    772
94  Arg Asp Ile Cys Ile Asp Phe Ser Glu Leu Ile Ser Gln Tyr Ser Asp
95                235                 240                 245
97  gag gag gag atc cag cat gtg gta gag gtg att caa aat tcc acg gcc    820
98  Glu Glu Glu Ile Gln His Val Val Glu Val Ile Gln Asn Ser Thr Ala
99                250                 255                 260
101 aaa gtc atc gtg gtt ttc tcc agt ggc cca gat ctt gag ccc ctc atc    868
102 Lys Val Ile Val Val Phe Ser Ser Gly Pro Asp Leu Glu Pro Leu Ile
103 265                 270                 275                 280
105 aag gag att gtc cgg cgc aat atc acg ggc aag atc tgg ctg gcc agc    916
106 Lys Glu Ile Val Arg Arg Asn Ile Thr Gly Lys Ile Trp Leu Ala Ser
107                285                 290                 295
109 gag gcc tgg gcc agc tcc tcc ctg atc gcc atg cct cag tac ttc cac    964
110 Glu Ala Trp Ala Ser Ser Ser Leu Ile Ala Met Pro Gln Tyr Phe His
111                300                 305                 310
113 gtg gtt ggc ggc acc att gga ttc gct ctg aag gct ggg cag atc cca    1012
114 Val Val Gly Gly Thr Ile Gly Phe Ala Leu Lys Ala Gly Gln Ile Pro
115                315                 320                 325
117 ggc ttc cgg gaa ttc ctg aag aag gtc cat ccc agg aag tct gtc cac    1060
118 Gly Phe Arg Glu Phe Leu Lys Lys Val His Pro Arg Lys Ser Val His
119 330                 335                 340
121 aat ggt ttt gcc aag gag ttt tgg gaa gaa aca ttt aac tgc cac ctc    1108
122 Asn Gly Phe Ala Lys Glu Phe Trp Glu Glu Thr Phe Asn Cys His Leu
123 345                 350                 355                 360
125 caa gaa ggt gca aaa gga cct tta cct gtg gac acc ttt ctg aga ggt    1156
126 Gln Glu Gly Ala Lys Gly Pro Leu Pro Val Asp Thr Phe Leu Arg Gly
127                365                 370                 375
129 cac gaa gaa agt ggc gac agg ttt agc aac agc tcg aca gcc ttc cga    1204
130 His Glu Glu Ser Gly Asp Arg Phe Ser Asn Ser Ser Thr Ala Phe Arg
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                RAW SEQUENCE LISTING              DATE: 12/17/2001
                PATENT APPLICATION: US/10/002,854  TIME: 20:19:56

                Input Set : A:\Pto.amc
                Output Set: N:\CRF3\12172001\J002854.raw

131             380                 385                 390
133  ccc ctc tgt aca ggg gat gag aac atc agc agt gtc gag acc cct tac    1252
134  Pro Leu Cys Thr Gly Asp Glu Asn Ile Ser Ser Val Glu Thr Pro Tyr
135          395                 400                 405
137  ata gat tac acg cat tta cgg ata tcc tac aat gtg tac tta gca gtc    1300
138  Ile Asp Tyr Thr His Leu Arg Ile Ser Tyr Asn Val Tyr Leu Ala Val
139          410                 415                 420
141  tac tcc att gcc cac gcc ttg caa gat ata tat acc tgc tta cct ggg    1348
142  Tyr Ser Ile Ala His Ala Leu Gln Asp Ile Tyr Thr Cys Leu Pro Gly
143  425                 430                 435                 440
145  aga ggg ctc ttc acc aat ggc tcc tgt gca gac atc aag aag gtt gag    1396
146  Arg Gly Leu Phe Thr Asn Gly Ser Cys Ala Asp Ile Lys Lys Val Glu
147              445                 450                 455
149  gcg tgg cag gtc ctg aag cac cta cgg cat cta aac ttt aca aac aat    1444
150  Ala Trp Gln Val Leu Lys His Leu Arg His Leu Asn Phe Thr Asn Asn
151          460                 465                 470
153  atg ggg gag cag gtg acc ttt gat gag tgt ggt gac ctg gtg ggg aac    1492
154  Met Gly Glu Gln Val Thr Phe Asp Glu Cys Gly Asp Leu Val Gly Asn
155          475                 480                 485
157  tat tcc atc atc aac tgg cac ctc tcc cca gag gat ggc tcc atc gtg    1540
158  Tyr Ser Ile Ile Asn Trp His Leu Ser Pro Glu Asp Gly Ser Ile Val
159          490                 495                 500
161  ttt aag gaa gtc ggg tat tac aac gtc tat gcc aag aag gga gaa aga    1588
162  Phe Lys Glu Val Gly Tyr Tyr Asn Val Tyr Ala Lys Lys Gly Glu Arg
163  505                 510                 515                 520
165  ctc ttc atc aac gag gag aaa atc ctg tgg agt ggg ttc tcc agg gag    1636
166  Leu Phe Ile Asn Glu Glu Lys Ile Leu Trp Ser Gly Phe Ser Arg Glu
167              525                 530                 535
169  gtg ccc ttc tcc aac tgc agc cga gac tgc ctg gca ggg acc agg aaa    1684
170  Val Pro Phe Ser Asn Cys Ser Arg Asp Cys Leu Ala Gly Thr Arg Lys
171              540                 545                 550
173  ggg atc att gag ggg gag ccc acc tgc tgc ttt gag tgt gtg gag tgt    1732
174  Gly Ile Ile Glu Gly Glu Pro Thr Cys Cys Phe Glu Cys Val Glu Cys
175              555                 560                 565
177  cct gat ggg gag tat agt gat gag aca gat gcc agt gcc tgt aac aag    1780
178  Pro Asp Gly Glu Tyr Ser Asp Glu Thr Asp Ala Ser Ala Cys Asn Lys
179          570                 575                 580
181  tgc cca gat gac ttc tgg tcc aat gag aac cac acc tcc tgc att gcc    1828
182  Cys Pro Asp Asp Phe Trp Ser Asn Glu Asn His Thr Ser Cys Ile Ala
183  585                 590                 595                 600
185  aag gag atc gag ttt ctg tcg tgg acg gag ccc ttt ggg atc gca ctc    1876
186  Lys Glu Ile Glu Phe Leu Ser Trp Thr Glu Pro Phe Gly Ile Ala Leu
187              605                 610                 615
189  acc ctc ttt gcc gtg ctg ggc att ttc ctg aca gcc ttt gtg ctg ggt    1924
190  Thr Leu Phe Ala Val Leu Gly Ile Phe Leu Thr Ala Phe Val Leu Gly
191              620                 625                 630
193  gtg ttt atc aag ttc cgc aac aca ccc att gtc aag gcc acc aac cga    1972
194  Val Phe Ile Lys Phe Arg Asn Thr Pro Ile Val Lys Ala Thr Asn Arg
195              635                 640                 645
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197  gag ctc tcc tac ctc ctc ctc ttc tcc ctg ctc tgc tgc ttc tcc agc    2020
198  Glu Leu Ser Tyr Leu Leu Leu Phe Ser Leu Leu Cys Cys Phe Ser Ser
199      650                 655                 660
201  tcc ctg ttc ttc atc ggg gag ccc cag gac tgg acg tgc cgc ctg cgc    2068
202  Ser Leu Phe Phe Ile Gly Glu Pro Gln Asp Trp Thr Cys Arg Leu Arg
203  665                 670                 675                 680
205  cag ccg gcc ttt ggc atc agc ttc gtg ctc tgc atc tca tgc atc ctg    2116
206  Gln Pro Ala Phe Gly Ile Ser Phe Val Leu Cys Ile Ser Cys Ile Leu
207                      685                 690                 695
209  gtg aaa acc aac cgt gtc ctc ctg gtg ttt gag gcc aag atc ccc acc    2164
210  Val Lys Thr Asn Arg Val Leu Leu Val Phe Glu Ala Lys Ile Pro Thr
211                  700                 705                 710
213  agc ttc cac cgc aag tgg tgg ggg ctc aac ctg cag ttc ctg ctg gtt    2212
214  Ser Phe His Arg Lys Trp Trp Gly Leu Asn Leu Gln Phe Leu Leu Val
215      715                 720                 725
217  ttc ctc tgc acc ttc atg cag att gtc atc tgt gtg atc tgg ctc tac    2260
218  Phe Leu Cys Thr Phe Met Gln Ile Val Ile Cys Val Ile Trp Leu Tyr
219      730                 735                 740
221  acc gcg ccc ccc tca agc tac cgc aac cag gag ctg gag gat gag atc    2308
222  Thr Ala Pro Pro Ser Ser Tyr Arg Asn Gln Glu Leu Glu Asp Glu Ile
223  745                 750                 755                 760
225  atc ttc atc acg tgc cac gag tcc ctc atg gcc ctg ggc ttc ctg        2356
226  Ile Phe Ile Thr Cys His Glu Ser Leu Met Ala Leu Gly Phe Leu
227                  765                 770                 775
229  atc ggc tac acc tgc ctg ctg gct gcc atc tgc ttc ttc ttt gcc ttc    2404
230  Ile Gly Tyr Thr Cys Leu Leu Ala Ala Ile Cys Phe Phe Phe Ala Phe
231                  780                 785                 790
233  aag tcc cgg aag ctg ccg gag aac ttc aat gaa gcc aag ttc atc acc    2452
234  Lys Ser Arg Lys Leu Pro Glu Asn Phe Asn Glu Ala Lys Phe Ile Thr
235      795                 800                 805
237  ttc agc atg ctc atc ttc ttc atc gtc tgg atc tcc ttc att cca gcc    2500
238  Phe Ser Met Leu Ile Phe Phe Ile Val Trp Ile Ser Phe Ile Pro Ala
239      810                 815                 820
241  tat gcc agc acc tat ggc aag ttt gtc tct gcc gta gag gtg att gcc    2548
242  Tyr Ala Ser Thr Tyr Gly Lys Phe Val Ser Ala Val Glu Val Ile Ala
243  825                 830                 835                 840
245  atc ctg gca gcc agc ttt ggc ttg ctg gcg tgc atc ttc ttc aac aag    2596
246  Ile Leu Ala Ala Ser Phe Gly Leu Leu Ala Cys Ile Phe Phe Asn Lys
247                      845                 850                 855
249  acc tac atc att ctc ttc aag cca tcc cgc aac acc atc gag gag gtg    2644
250  Thr Tyr Ile Ile Leu Phe Lys Pro Ser Arg Asn Thr Ile Glu Glu Val
251                  860                 865                 870
253  cgt tgc agc agc acc gca cgt cac gct ttc aag gtg gct gcc cgg gcc acg 2692
254  Arg Cys Ser Ser Thr Ala Arg His Ala Phe Lys Val Ala Ala Arg Ala Thr
255      875                 880                 885
257  ctg cgc cgc agc aac gtc tcc cgc aag cgg tcc agc agc ctt gga ggc    2740
258  Leu Arg Arg Ser Asn Val Ser Arg Lys Arg Ser Ser Ser Leu Gly Gly
259      890                 895                 900
261  tcc acg gga tcc acc ccc tcc tcc tcc atc agc agc aag agc aac agc    2788
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                    RAW SEQUENCE LISTING          DATE: 12/17/2001
                    PATENT APPLICATION:  US/10/002,854   TIME: 20:19:56

                    Input Set : A:\Pto.amc
                    Output Set: N:\CRF3\12172001\J002854.raw

262  Ser Thr Gly Ser Thr Pro Ser Ser Ser Ile Ser Ser Lys Ser Asn Ser
263  905                     910                 915                 920
265  gaa gac cca ttc cca cag ccc gag agg cag aag cag cag cag ccg ctg   2836
266  Glu Asp Pro Phe Pro Gln Pro Glu Arg Gln Lys Gln Gln Gln Pro Leu
267                      925                 930                 935
269  gcc cta acc cag caa gag cag caa cag cag ccc ctg acc ctc cca cag   2884
270  Ala Leu Thr Gln Gln Glu Gln Gln Gln Gln Pro Leu Thr Leu Pro Gln
271                  940                 945          .        950
273  cag caa cga tct cag cag cag ccc aga tgc aag cag aag gtc atc ttt   2932
274  Gln Gln Arg Ser Gln Gln Gln Pro Arg Cys Lys Gln Lys Val Ile Phe
275              955                 960                 965
277  ggc agc ggc acg gtc acc ttc tca ctg agc ttt gat gag cct cag aag   2980
278  Gly Ser Gly Thr Val Thr Phe Ser Leu Ser Phe Asp Glu Pro Gln Lys
279          970                 975                 980
281  aac gcc atg gcc cac agg aat tct acg cac cag aac tcc ctg gag gcc   3028
282  Asn Ala Met Ala His Arg Asn Ser Thr His Gln Asn Ser Leu Glu Ala
283  985                 990                 995                 1000
285  cag aaa gac agc agc gat acg ctg acc cga cac cag cca tta ctc ccg ctg   3076
286  Gln Lys Ser Ser Asp Thr Leu Thr Arg His Gln Pro Leu Leu Pro Leu
287              1005                1010                1015
289  cag tgc ggg gaa acg gac tta gat ctg acc gtc cag gaa aca ggt ctg   3124
290  Gln Cys Gly Glu Thr Asp Leu Asp Leu Thr Val Gln Glu Thr Gly Leu
291              1020                1025                1030
293  caa gga cct gtg ggt gga gac cag cgg cca gag gtg gag gac cct gaa   3172
294  Gln Gly Pro Val Gly Gly Asp Gln Arg Pro Glu Val Glu Asp Pro Glu
295          1035                1040                1045
297  gag ttg tcc cca gca ctt gta gtg tcc agt tca cag agc ttt gtc atc   3220
298  Glu Leu Ser Pro Ala Leu Val Val Ser Ser Ser Gln Ser Phe Val Ile
299  1050                1055                1060
301  agt ggt gga ggc agc act gtt aca gaa aac gta gtg aat tca           3262
302  Ser Gly Gly Gly Ser Thr Val Thr Glu Asn Val Val Asn Ser
303  1065                1070                1075
305  taaaatggaa ggagaagact gggctaggga gaatgcagag aggtttcttg gggtcccagg   3322
306  gatgaggaat cgccccagac tcctttcctc tgaggaaga                        3361
308  <210> SEQ ID NO: 2
309  <211> LENGTH: 1078
310  <212> TYPE: PRT
311  <213> ORGANISM: Homo sapiens
313  <220> FEATURE:
314  <221> NAME/KEY: PEPTIDE
315  <222> LOCATION: (1)...(1078)
316  <223> OTHER INFORMATION: Ca-sensing Receptor
318  <400> SEQUENCE: 2
319  Met Ala Phe Tyr Ser Cys Cys Trp Val Leu Leu Ala Leu Thr Trp His
320  1                   5                   10                  15
321  Thr Ser Ala Tyr Gly Pro Asp Gln Arg Ala Gln Lys Lys Gly Asp Ile
322                  20                  25                  30
323  Ile Leu Gly Gly Leu Phe Pro Ile His Phe Gly Val Ala Ala Lys Asp
324              35                  40                  45
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VERIFICATION SUMMARY   DATE: 12/17/2001
PATENT APPLICATION: US/10/002,854   TIME: 20:19:57

Input Set : A:\Pto.amc
Output Set: N:\CRF3\12172001\J002854.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date